

1. An isolated or recombinant polypeptide comprising an amino acid sequence encoded hepatitis C alternate reading frame.
14. A vaccine composition for preventing hepatitis C infection in a subject comprising the polypeptide of claim 1.
24. An antibody which binds to a polypeptide of claim 1.
25. A kit for detecting a hepatitis C infection comprising the polypeptide of claim 1.
26. A kit for detecting a hepatitis C infection comprising an antibody to the polypeptide of claim 1.

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- ✓ 28. **(Amended)** A method of diagnosing Hepatitis C virus (HCV) infection, comprising detecting the presence or absence of antibodies in the body fluid of a subject, wherein the antibodies react with a polypeptide comprising an amino acid sequence encoded by an HCV alternate reading frame, and wherein the presence of the antibodies is indicative of an infection with HCV.

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- 29. **(Amended)** A method of diagnosing Hepatitis C virus (HCV) infection, comprising detecting the presence or absence of a polypeptide in the body fluid or cells of a subject, wherein the polypeptide comprises an amino acid sequence encoded by an HCV alternate reading frame, and wherein the presence of the polypeptide is indicative of an infection with HCV.

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30. A method for identifying a compound which interacts with the polypeptide of claim 1, comprising:
- contacting said polypeptide with a compound in a cell-free system under conditions which allow interaction of the compound with the polypeptide such that a complex is formed;

separating the compounds which do not form complexes with the polypeptide from those which do form complexes with the polypeptide; and
isolating and identifying the compounds which form complexes with the polypeptide to thereby identify a compound which interacts with the polypeptide of claim 1.

31. **(Amended)** A method of diagnosing HCV infection comprising detecting the presence or absence of an HCV alternate reading frame polypeptide or detecting the presence or absence of antibodies which bind to an HCV alternate reading frame polypeptide in the body fluid or cells of a subject, wherein the presence of the HCV alternate reading frame polypeptide or antibodies which bind to the HCV alternate reading frame polypeptide is indicative of an infection with HCV.

Please add the following new claims:

--36. **(New)** The method of claim 29, wherein the presence or absence of the polypeptide is detected by contacting a test sample comprising body fluid or cells of a subject with an antibody under conditions which allow the binding of the polypeptide to the antibody and wherein the binding of the antibody to the polypeptide in the sample indicates the presence of an HCV alternate reading frame polypeptide.

37. **(New)** The method of claim 28, wherein the presence or absence of antibodies is detected by contacting a test sample comprising body fluid of a subject with the polypeptide under conditions which allow the binding of the polypeptide to the antibody and wherein the binding of the polypeptide to the antibody in the sample indicates the presence of an HCV alternate reading frame polypeptide.

38. (New) The method of claim 31, wherein the polypeptide comprises an amino acid sequence encoded by a reading frame corresponding to the reading frame of SEQ ID NO:1 in which the first nucleotide of SEQ ID NO:1 is the first nucleotide of a codon. *only*

39. (New) The method of claim 31, wherein the polypeptide is at least about 8 amino acids to at least about 100 amino acids in length.

40. (New) The method of claim 31, wherein the polypeptide is at least about 14 amino acids to at least about 30 amino acids in length.

41. (New) The method of claim 31, wherein the entire polypeptide is encoded by a reading frame +1 or +2 to the standard hepatitis C reading frame.

B3 42. (New) The method of claim 31, wherein the polypeptide comprises an amino acid sequence at least about 60% -70% identical to the amino acid sequence shown in SEQ ID NO:2 using FASTA alignment.

43. (New) The method of claim 31, wherein the polypeptide comprises an amino acid sequence at least about 90% identical to the amino acid sequence shown in SEQ ID NO:2 using FASTA alignment.

44. (New) The method of claim 31, wherein the polypeptide comprises at least 8 contiguous amino acids of SEQ ID NO:2.

~ 45. (New) The method of claim 31, wherein the polypeptide comprises at least 8 contiguous amino acids of SEQ ID NO:9.

46. (New) The method of claim 31, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes under high stringency to a nucleic acid molecule having the nucleotide sequence shown in SEQ ID NO:1. *1 2 1 1 2 1*